

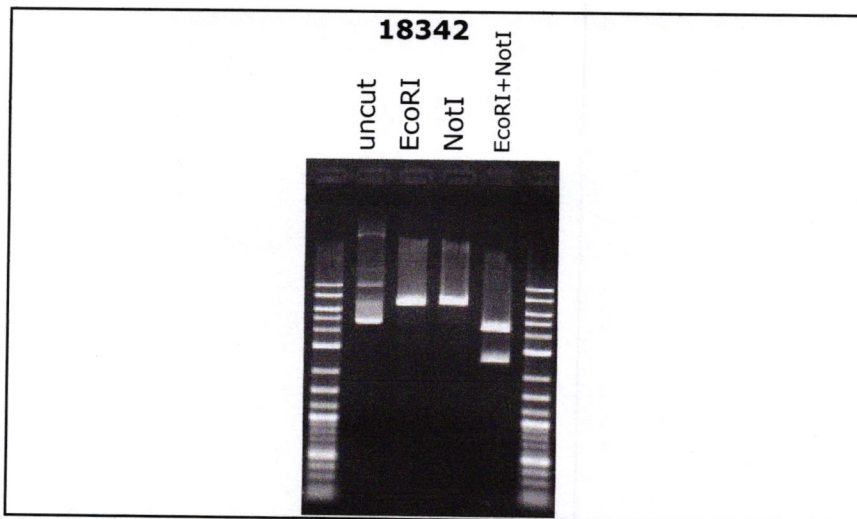
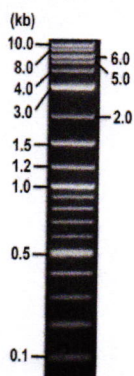


**RIKEN DNA BANK**

clone name : pMK419 (GAL-OsTIR1F74G)

- Clone ID : RDB\_18342
- Lot : 18342\_B0Gf
- DNA Concentration : 25 nanogram/microliter
- Volume : 40 microliter
- Form : DNA solution in TE buffer
- Host : DH5 alpha
- Culture : LB medium
- Antibiotics : 100 microgram/ml Ampicillin
- Purification : QIAGEN QIAprep Spin Miniprep kit
- Digestion by restriction enzyme

1 kb Plus DNA Ladder  
(NEB#N3200L),  
250 ng/well



Electrophoresis : 100 nanogram DNA per lane ; 1% agarose gel , 1 x TAE Buffer

Restriction enzyme	Expected size of fragment
<b>EcoRI</b>	<b>6.9</b> kbp
<b>NotI</b>	<b>6.9</b> kbp
<b>EcoRI+NotI</b>	<b>4.3, 2.5</b> kbp
	kbp

● Confirmation of the insertion sequence

Please be sure to check our sequence analysis results before your request.

Sequence name	Primer ID	Primer name	Confirmed feature
Sequence - A	Pr0739	pUC-CAPbs_up_F2	insert 5'(GAL1-10 pro)
Sequence - B	Pr0544	pBAC_lac_F	insert 3'(OsTIR1(F74G) 3')
Sequence - C	Pr0030	GAL1pro_F	insert mid(GAL1-10 pro,OsTIR1(F74G) 5')
Sequence - D	Pr0170	URA3pro_F	URA3 pro, URA3 5'
Sequence - E	-	-	-
Sequence - F	-	-	-
Sequence - G	-	-	-
Sequence - H	-	-	-

APPROVED BY :













S/N G:174 A:208 T:250 C:195

primer name  $\beta$  : pBAC\_lac\_F

D07105B1\_B0Gf\_1\_pBAC\_lac\_F

Mar 24, 2021 05:23PM, JST

KB.bcp

5'-CGCCAGGGTTTCCACAGTCACGAC-3'

KB\_3500\_POP7\_BDTv3.mob

Mar 24, 2021 05:50PM, JST

KB 1.4.1.8

Cap:22

Pts 1461 to 13489 Pk1 Loc:1438

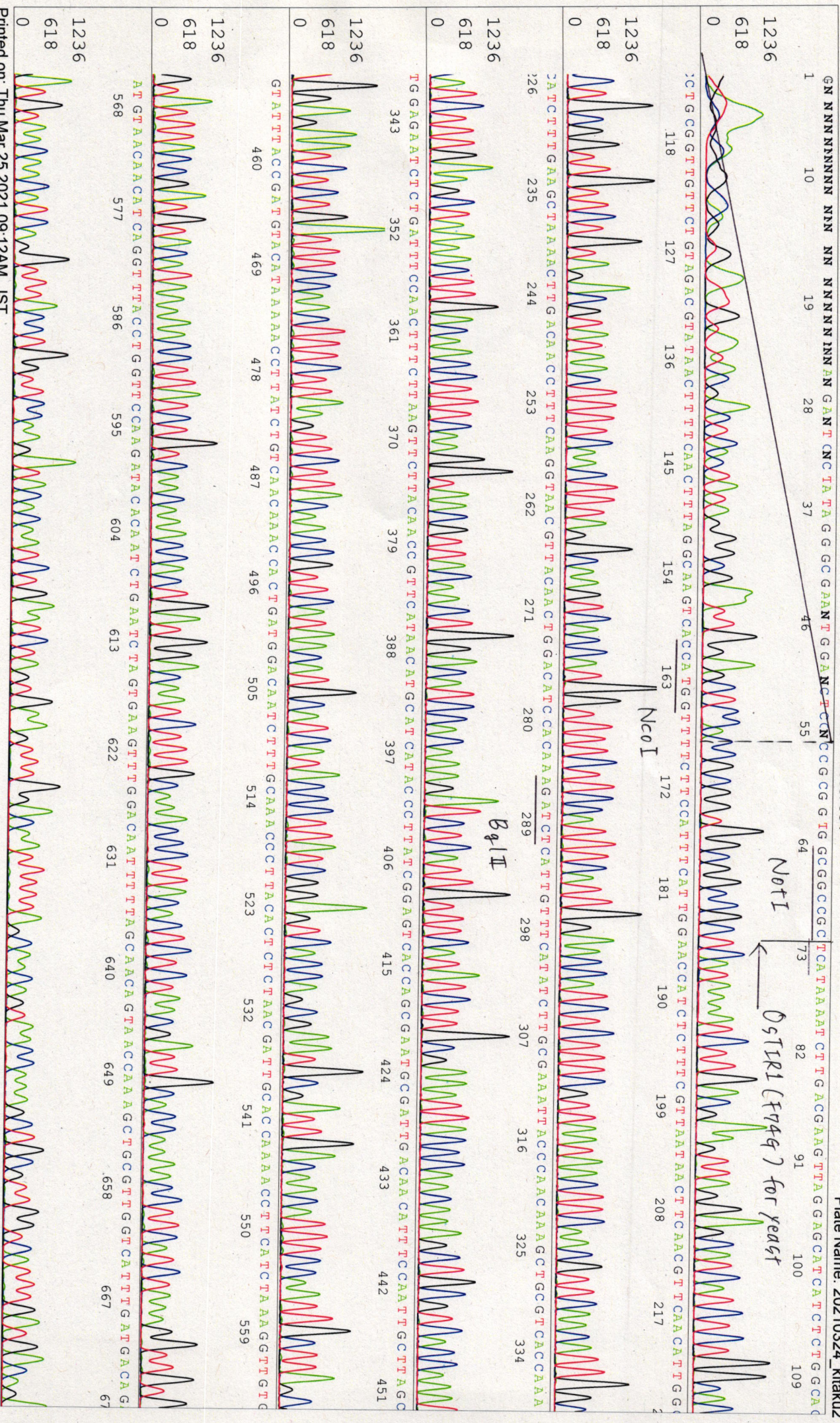
Spacing: 11.95 Pts/Panel1350

Version 6.0

HISQV Bases: 934

Version 6.0

Plate Name: 20210324\_kitaku2

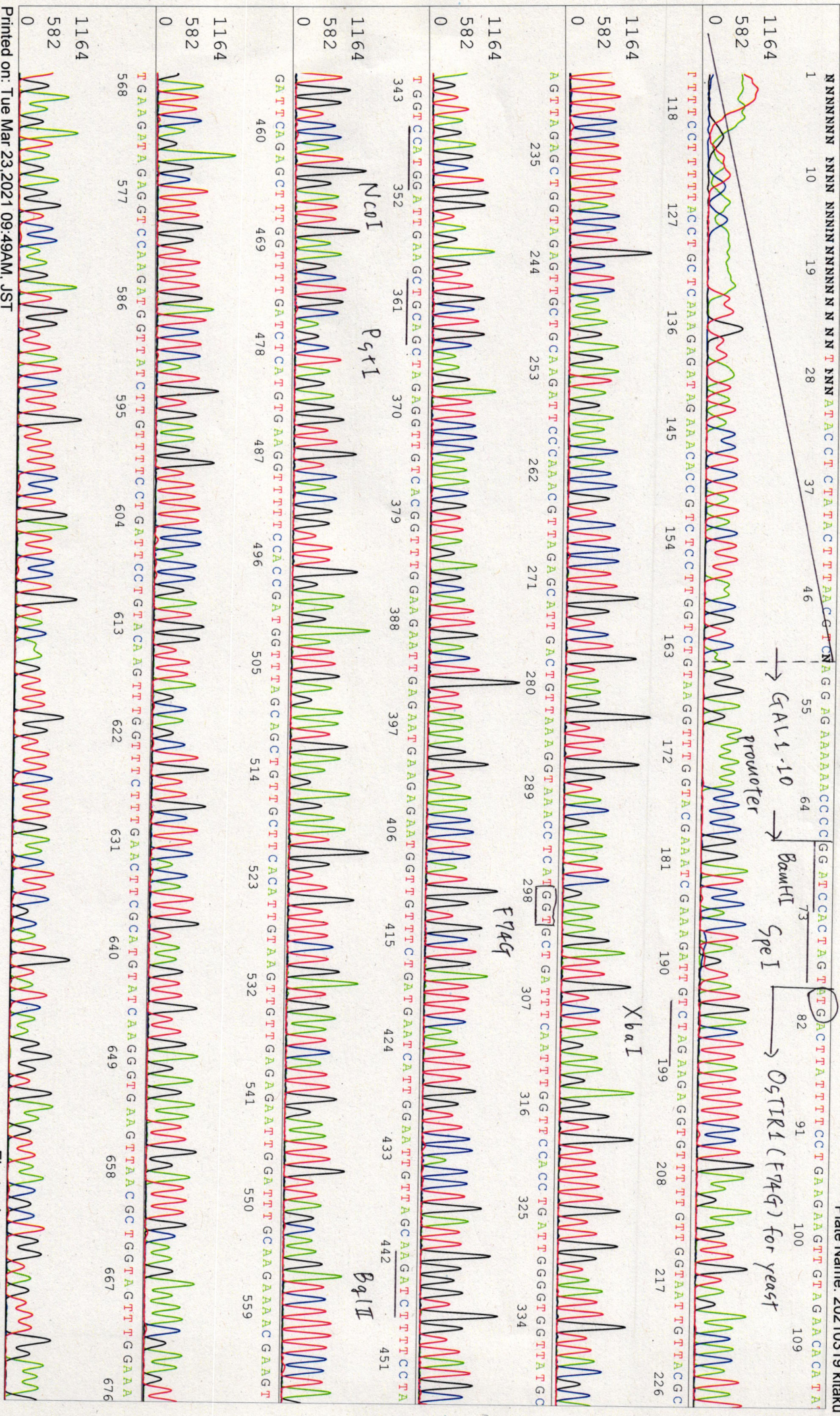








primer name C : GAL1pro\_F2  
5'-TGCAAAAACCTGCATAACCAC-3'













GGTTGATTATGACCA CCGGGTGTGGGTTTA GAT GACAAAGGGAGACGCCAT TGGGTCAACAGTATA GAAACCGTGGATGAN GTGGTCTCTTACAGGATCTGACAT TATTATTGNTG

685 694 703 712 721 730 739 748 757 766 775 784  
GAA GAG AN TATT TGC AAA GGGA GGAN GC TAAN GTA GAG GGT GAAN GT TAC AGA AAN CAN GCT GGGA AGCA TATT TGA GA AGAN GCC GGCA GCAAA ACT NAAAAA CT

901 910 919 928 937 946 955 964 973 982 991 1000  
GTATTATA G TNAATGNATGTATAC TNAACCTCNCAAA TTANAGCTTCNNNTTNAT TATATCA GTTATTANCCNA TGGCNGTGCNAA NANCNNNNN ANGCNNNN N

1009 1018 1027 1036 1045 1054 1063 1072 1081 1090  
NNN AAAANNNN N C N N C N N N A A N T N G N A N N C N N N N T T N G N N A A N

1099 1108 1117 1126 1135 1144 1153  
N N

1162 1171 1180  
N N

URA3

